

SEQUENCE LISTING

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(1) GENERAL INFORMATION

- (i) APPLICANT: O'Gorman, Steve
Wahl, Geoffrey
- (ii) TITLE OF THE INVENTION: Site-Specific Recombination
in Eukaryotes and Constructs Useful Therefor
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Gray Cary Ware & Freidenrich
(B) STREET: 4365 Executive Drive, Suite 1600
(C) CITY: San Diego
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92121
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows DEMONSTRATION Version 2.0D
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Reiter, Stephen E
(B) REGISTRATION NUMBER: 31,192
(C) REFERENCE/DOCKET NUMBER: Salk2190
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 619-677-1409
(B) TELEFAX: 619-677-1465
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1022 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGGAGCAAA	AGCTGATTTC	TGAGGGAGGAT	CTGGGGAGGAC	CCAAGAAGAA	GAGGAAGGTG	60
TCCAATTAC	TGACCGTACA	CCAAAATTTG	CCTGCATTAC	CGGTCGATGC	AACGAGTGAT	120
GAGGTTCGCA	AGAACCTGAT	GGACATGTTC	AGGGATCGCC	AGGCCTTTTC	TGAGCATACC	180
TGGAAAATGC	TTCTGTCCGT	TTGCCGGTCG	TGGGCCGGCAT	GGTGCAAGTG	AATAACCGGA	240
AATGGTTTCC	CGCAGAACCT	GAAGATGTTC	GCGATTATCT	TCTATATCTT	CAGGCGCGCG	300
GTCTGGCAGT	AAAAACTATC	CAGCAACATT	TGGGCCAGCT	AAACATGCTT	CATCGTCGGT	360
CCGGGCTGCC	ACGACCAAGT	GACAGCAATG	CTGTTTCACT	GGTTATGC GG	CGGATCCGAA	420
AAGAAAACGT	TGATGCCGGT	GAACGTGCAA	AACAGGCTCT	AGCGTTCGAA	CGCACTGATT	480
TCGACCAGGT	TCGTTCACTC	ATGGAAAATA	GCGATCGCTG	CCAGGATATA	CGTAATCTGG	540
CATTCTGGG	GATTGTTAT	AACACCCCTGT	TACGTATAGC	CGAAATTGCC	AGGATCAGGG	600
TTAAAGATAT	CTCACGTA	GACGGTGGGA	GAATGTTAAT	CCATATTGGC	AGAACGAAAA	660
CGCTGGTTAG	CACCGCAGGT	GTAGAGAAGG	CACTTAGCCT	GGGGGTAACT	AAACTGGTCG	720
ACCGATGGAT	TTCGGTCTCT	GGTGTAGCTG	ATGATCCGAA	TAAC TACCTG	TTTGCCCCGG	780
TCAGAAAAAA	TGGTGGTGC	GCGCCATCTG	CCACCA GCCA	GCTATCAACT	CGCGCCCTGG	840
AAGGGATT	TGAAGCAACT	CATCGATTGA	TTTACGGCGC	TAAGGATGAC	TCTGGTCAGA	900
GATAACCTGGC	CTGGTCTGG	CACAGTGCCC	GTGTCGGAGC	CGCGCGAGAT	ATGGCCCGCG	960
CTGGAGTTTC	AATACCGGAG	ATCATGCAAG	CTGGTGGCTG	GACCAATGTA	AATATTGTCA	1020
TG						1022

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTCTAGTAAT GTCCAACACC TCCCTCAGT

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCTGAGCCA GCTCCGGCC AAGCCAGCAC C

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTCTAGTAAT	GTCCAACACC	TCCCTCAGTC	CAAACACTGC	TCTGCATCCA	TGTGGCTCCC	60
ATTTTATACT	GAAGCACTTG	ATGGGGCCTC	AATGTTTTAC	TAGAGCCCAC	CCCCCTGCAA	120
CTCTGAGACC	CTCTGGATT	GTCTGTCA	GCCTCACTGG	GGCGTTGGAT	AATTCTTAA	180
AAGGTCAAGT	TCCCTCAGCA	GCATTCTCTG	AGCAGTCTGA	AGATGTTGTC	TTTCACAGTT	240
ACAAATCCAT	GTGGCTGTT	CACCCACCTG	CCTGGCCTTG	GGTTATCTAT	CAGGACCTAG	300
CCTAGAAGCA	GGTGTGTGGC	ACTTAACACC	TAAGCTGAGT	GACTAACTGA	ACACTCAAGT	360
GGATGCCATC	TTTGTCACTT	CTTGACTGTG	ACACAAGCAA	CTCCTGATGC	CAAAGCCCTG	420

CCCACCCCTC	TCATGCCCAT	ATTTGGACAT	GGTACAGGTC	CTCACTGGCC	ATGGTCTGTG	480
AGGTCTGGT	CCTCTTGAC	TTCATAATT	CTAGGGGCCA	CTAGTATCTA	TAAGAGGAAG	540
AGGGTGCTGG	CTCCCAGGCC	ACAGCCCACA	AAATTCCACC	TGCTCACAGG	TTGGCTGGCT	600
CGACCCAGGT	GGTGTCCCCT	GCTCTGAGCC	AGCTCCCGGC	CAAGCCAGCA	CC	652

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATAACTTCGT ATAGCATAACA TTATACGAAG TTAT

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(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 86 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCCGGGATCA	ATTCACCATG	GGAATAACTT	CGTATAGCAT	ACATTATACG	AAGTTATGGA	60
TCCGCCGCTA	TCAGGACATA	GC	GTG			86